



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/820,816
Source: 1 FWS
Date Processed by STIC: 8/20/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

~~TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER~~
~~VERSION 4.2 PROGRAM ACCESSIBLE THROUGH THE U.S. PATENT AND~~
~~TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:~~

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box-1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/820,816

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ **Wrapped Nucleics**
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☒ **Misaligned Amino
Numbering** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☒ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ **Variable Length** Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ **PatentIn 2.0
"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ **Skipped Sequences
(OLD RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ **Skipped Sequences
(NEW RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☐ **Use of n's or Xaa's
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ **Invalid <213>
Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ **Use of <220>** Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ **PatentIn 2.0
"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ **Misuse of n/Xaa** "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

RAW SEQUENCE LISTING

DATE: 08/20/2004

PATENT APPLICATION: US/10/820,816

TIME: 11:11:12

Input Set : A:\PTO.LM.txt

Output Set: N:\CRF4\08202004\J820816.raw

*IMPORTANT: see item 4
on Enr summary
sheet*

3 <110> APPLICANT: HOVANESSIAN, Ara
4 BRIAND, Jean-Paul
5 MULLER, Sylviane
6 KRUST, Bernard
7 SVAB, Josette
8 SAID, Elias
10 <120> TITLE OF INVENTION: NOVEL SYNTHETIC PEPTIDE VACCINES FOR HIV: THE CBD
11 EPITOPE AS AN EFFECTIVE IMMUNOGEN TO ELICIT BROADLY
12 NEUTRALIZING ANTIBODIES AGAINST HIV
14 <130> FILE REFERENCE: B5602A - JAZ/KN (I.PASTEUR & CNRS)
C--> 16 <140> CURRENT APPLICATION NUMBER: US/10/820,816
17 <141> CURRENT FILING DATE: 2004-04-09
19 <150> PRIOR APPLICATION NUMBER: EP03290919.4
20 <151> PRIOR FILING DATE: 2003-04-11
22 <160> NUMBER OF SEQ ID NOS: 21
24 <170> SOFTWARE: PatentIn Ver. 2.1

pp 1-3

**Does Not Comply
Corrected Diskette Needed**

ERRORED SEQUENCES

368 <210> SEQ ID NO: 21
369 <211> LENGTH: 45
370 <212> TYPE: DNA
371 <213> ORGANISM: Artificial Sequence
373 <220> FEATURE:
374 <223> OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
375 of SEQ ID No. 2
377 <400> SEQUENCE: 21
378 ctggaacaga tttggaataa catgacctgg atgcagtggg acaaaa
E--> 384 6
E--> 390 2
E--> 396 1
E--> 402 7
E--> 407 1

delete

Nucleic
Nucleic Acid

45

*(please
try to
be more
specific
about source
of genetic
material)*

10/820,816 2

Per 1.823 d
Sequence rules, wherever
"Xaa" or "n" is shown, please
show locations on <2227 line.

<210> 11
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Variant of SEQ
ID No. 2 in which X is any amino acid, n is 0 to
20 and m is 0 to 20

<400> 11
Xaa Leu Glu Gln Ile Trp Asn Asn Met Thr Trp Met Gln Trp Asp Lys
1 5 10 15

Xaa

<210> 12
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Variant of SEQ
ID No. 3 in which X is any amino acid, n is 0 to
20 and m is 0 to 20

same errors

<400> 12
Xaa Leu Thr Pro Asp Trp Asn Asn Met Thr Trp Gln Glu Trp Glu Arg
1 5 10 15

Xaa

By "n", do you
mean Asparagine?

By "m", do you mean
Methionine?

Try I: variable
length is not
permitted. An
amino acid, as shown,
can only represent
a single amino
acid. Show

the maximum
number of

the amino acid
and explain in

<2207-22237 section
that some may

be missing

(e.g., display 20

Asn's; display 20

Met's

VARIABLE LOCATION SUMMARY

PATENT APPLICATION: US/10/820,816

DATE: 08/20/2004

TIME: 11:11:14

Input Set : A:\PTO.LM.txt

Output Set: N:\CRF4\08202004\J820816.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:1; Xaa Pos. 2,3,4,5,7,8

Seq#:11; Xaa Pos. 1,17

Seq#:12; Xaa Pos. 1,17

Seq#:13; Xaa Pos. 5,10,13

Seq#:14; Xaa Pos. 5,10,13

Seq#:15; Xaa Pos. 7

Seq#:16; Xaa Pos. 9

Seq#:17; Xaa Pos. 7

Seq#:18; Xaa Pos. 9

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/820,816

DATE: 08/20/2004

TIME: 11:11:14

Input Set : A:\PTO.LM.txt

Output Set: N:\CRF4\08202004\J820816.raw

L:16 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:36 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:1
 L:36 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:1
 L:36 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
 L:212 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:11
 L:212 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:11
 L:212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
 L:215 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:16
 L:231 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:12
 L:231 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:12
 L:231 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
 L:234 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:16
 L:251 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:13
 L:251 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:13
 L:251 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
 L:266 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:14
 L:266 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:14
 L:266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
 L:283 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:15
 L:283 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:15
 L:283 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
 L:300 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:16
 L:300 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:16
 L:300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
 L:319 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:17
 L:319 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:17
 L:319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
 L:336 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:18
 L:336 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:18
 L:336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
 L:384 M:254 E: No. of Bases conflict, this line has no nucleotides.
 L:390 M:254 E: No. of Bases conflict, this line has no nucleotides.
 L:396 M:254 E: No. of Bases conflict, this line has no nucleotides.
 L:402 M:254 E: No. of Bases conflict, this line has no nucleotides.
 L:407 M:254 E: No. of Bases conflict, this line has no nucleotides.